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1413.163 Million cell updates/sec
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Search completed: April 19, Job time: 43.7895 secs
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Best Local 9
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30-AUG-1993;
03-DEC-1993;
09-MAY-1994;
                                                                                                                                                                                                                                                                                                 Sequence 201 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated DNA encoding hek-L protein or its fusion products - useful as assay reagent or for carrying therapeutic and diagnostic compounds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ85888
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Total number of hits satisfying chosen parameters:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; C:
Mammalia; Eutheria; Primates; C:
1 (bases 1 to 1741)
Li,W.B., Gruber,C., Jessee,J. a:
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full-length cDNA clone
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BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
Bb: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                   GAACACCTGCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCC 657
                                                                                   GGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGG
                                                                                                                                                 ACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAG
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/mol_type="mRNA"
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/tissue_type="Adult brain"
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100.0%; Pr
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Pred. No. 6.2e-143;
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Scoring table:

Perfect score:

Run

OM nucleic -

ACCESSION VERSION

KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS

RESULT 1 CR607482

LOCUS DEFINITION

Result

Score

657 645 622.6 598.4 587.2

score

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ORIGIN
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Best Local Similarity
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BX419695
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301 ATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCAC 360
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                                                353 AACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCGCACAGCCCC 412
                                                                     241 AACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCC 300
                                                                                                                                        181 GGAGGCGGGCAGAGCAGTACGTGCTGCAGCTGAGCCGCAACGGCTACCGCACCTGC 240
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Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, web: www.genoscope.cns.fr
lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence belongs to sequence cluster 497.£
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODFO19DA12QP1&c=497.f.
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On May 13, 2003 this sequence version replaced gi:30654816.
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BX419695 Homo sapiens FETAL BRAIN Homo Sapiens CDNA Clone
CSODFO19YB24 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9606"
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/dev stage="fetal"
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vector. Library was not normalized."
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99.8%; Pred. No. 3.7e-140;
Live 0; Mismatches 0;
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Best Local (Matches 659		FEATURES Source	REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Db RESULT 3	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
ch 24.8%; Score 622.6; DB 1; Length 1100; 1 Similarity 99.4%; Pred. No. 6.5e-135; 555; Conservative 1; Mismatches 0; Indels 3; Gaps 3; 1 CTGCTGGCCCAAGGGCCGGAAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGC 60	/molther many was not normalized." /molther many was not normalized."	Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANÉE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Ist strand cDNA was primed with a Notl-oligo(dT) primer. Five prime into the Not I and EcoRV sites of the pcfWSpARF 6 vector. Library was not normalized. Library was constructed by Life Technologies, a for more information about this cluster, see Location/Qualifiers Oxganism. Not. 100 Oxganis	Tyota; Metazoa; Chordata; Ilia; Eutheria; Primates; Nases 1 to 1100 B., Gruber,C., Jessee,J. length cDNA libraries an b 13, 2001 this services	AL533153 N AL533153 Homo sapiens ADULT BRAIN Homo sapiens CDNA cione AL533153 AL533153 AL533153 AL533153 GI:45708058 Homo sapiens cluman)	481 ACTETECCCCAGTTCACCATGGGCCCCAATGTGAACATCACGTGGAAAACCCGGCAAACCCC 592 593 ACTETECCCCCAATTCACCATGGGCCCCAATGTGAACATCAACGTGCTGGAAGACCTTTGAC 540 GAACAACCCTCAAGTTCACCATGGGCCCCAATGTGAACATCAACGTGCTGGAAGACTTTGAC 541 GGAGAAACCCTCAAGTGCCCAAAGCTTGAAAACATCAACGTGCTGGAAGACTTTGAC 652 GAAGAACCCTCAAGTGCCCAAGCTTGAGAACAACAGCATCAGCGGGAACCAGCCCCAAACCG 653 GGAGAAACCCTCAGGTGCCCAAGCTTGAGAACAACAGCATCAGCGGGAACCAGCCCCAAACCG 660 GAACAACCTGCCCCTGGCCCTAGGCTTGAGAAGAGCATCAGCGGGAACCAGCCCCAAACCG 61 GAACACCTGCCCCTGGCCGTGGGCATCGCCTTCCTTCCTCATGACCGTTCTTTGGCCTCC 61 GAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACCTTCTTTGGCCTCC 657 GAACACCTGCCCTTGGCCGTGGGCATCGCCTTCTTCCTCATGACCTTCTTTGGCCTCC 658 GAACACCTGCCCTTGGCCGTGGGCATCGCCTTCTTCCTCATGACCTTCTTTGGCCTCC 659 GAACACCTGCCCTTGGCCGTGGGCATCGCCTTCTTCCTCATGACCTTCTTTGGCCTCC 650 GAACACCTGCCCTTGGCCGTGGGCATCGCCTTCTTCCTCATGACCTTCTTTGGCCTCC 651 GAACACCTGCCCTTGGCCGTGGGCATCGCCTTCTTCCTCATGACCTTCTTTGGCCTCC 652 GAACACCTGCCCTTGGCCGTGGGCATCGCCTTCTTCCTCATGACCTTCTTTTTTTT	413 ATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTC

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                                      Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY
Email: segref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                           Mammalia; Eutheria; Primates; Craniata; Vertebr
Mammalia; Eutheria; Primates; Catarrhini; Homin
1 (bases 1 to 726)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                       AL527972 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens CDNA Clone CSODC027YP19 5-PRIME, mRNA sequence.

AL527972 AL527972 AL527972.3 GI:45703058
EST.
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For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODC027CH10Qp1&c=497.f.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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full-length cDNA clone CSODI026YI24 of Homo sapiens (human).
CR597504

mRNA linear 4 of Placenta Cot

HTC 21-JUL-2004 25-normalized

CR597504.1 GI:50478311 HTC; CNSLT_cDNA.

sapiens sapiens

Bikaryota, Netazoa, Chordata; Craniata; Vertebrata; Riteleostomi, i. Names 1 to 1629) Iammala Enther; C.; Jessee, J. and Polayes, D. Contact: Feng Liang Email: fliangelifetech.com URL: Faraday Avenue pt. invitrogen.com/ Invitroden Corporation 1600 Densecope. Den	Query Match Best Local; Matches 58: Qy 66 Db 77 Qy 186; Db 137; Qy 246; Db 257; Db 317; Db 317; Db 317; Dc 36; Dc 377; Dc 426; Dc 4	REFERENCE AUTHORS TITLE JOURNAL REMARK REFERENCE AUTHORS TITLE JOURNAL COMMENT COMMENT FEATURES SOURCE
	Similarity 99.5%; Pred. No. 1.3e-126; COAGGACTGCCAGAGGGCTACAGGCTACAGGGCTACAGGGTGAACGACTGCAACGGTGAACGACTGCAACGGTGAACGACTGCAACGGTGAACGACCTGCAACGTGAACGACCTGCAACGTGAACGACCTGCAACGTGAACGACCTGCAACGTGAACGACCTGCAACGTGAACGACCTGCAACGTGAACGACTATCTGGATAT 13; IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Eukaryota, Metazoa; Chordata; Craniata; Verte 1 (bases 1 to 1629) Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Gruber, C., Jessee, J. and Polayes, D. Unpublished CDNA libraries and normalization http://fulllength.cDNA libraries and normalization http://fulllength.invitrogen.com/ Invitrogen contact: Feng Liang Email: fliang@lifetech. 2 (bases 1 to 1629) Direct Submission Submitted (20-UUL-2004) Genoscope - Centre Nat - Web: www.genoscope.cns.fr) end enriched, double-strand cDNA was primed with a NotI-oligo(dwas normalized. Library was constructed by Life was normalized. Library was constructed by Life into the Not I and EcoR V sites of the pcMvSpOl division of Invitrogen. 1. 1629 /organism="Homo sapiens" /blaxef="maxon:9606" /clone="CSODIO26YI24" /blasmid="pcMvSpORT_6" Cot 25-normalized"

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Search completed: April 19, 2005, 21:57:08 Job time : 3057.14 Secs

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HTC; CNSLT_cDNA.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished Contact: Feng Liang Email: fliang@lifetech. http://fulllength.invitrogen.com/ InVitroGen Faraday Avenue
                  GAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAA 660
                                                                               CTCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGA
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN003YL19"
/tissue_type="Adult brain"
/plasmid="pCMVSPORT_6"
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On May 13, 203-1.
Contact: Genoscope
Genoscope - Centre National de Sequencage
genoscope - Centre National de Sequencage
1 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pcMVspcmf vector. Library
was not normalized. Library was constructed by Life Technologies, a

This sequence belongs to sequence cluster 497.f
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/mol type="mRNA"
/db_xcef="taxon:9666"
/clone="CSOPPO19YB24"
/tissue_type="FETAL BRAIN"
/dev stage="fetal"
/note="Torgan: brain; Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end cloned into the Not I and EcoRy sites of the pCMVSPORT 6 and vector. Library was not normalized."
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; Pred. No. 2.8e-134;
M'ematches 0;
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Contact: Genoscope Genoscope Genoscope Centre National de Sequencage

Imail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
into the Not I and EcoRV sites of the pCMVSSPAT of vector. Library
was not normalized. Library was constructed by Life Technologies, a

Es http://www.genoscope.cns.fr
into the Not I and EcoRV sites of the pCMVSSPAT of vector. Library
was not normalized. Library was constructed by Life Technologies, a

http://www.genoscope.cns.fr
control

Location/Oualifiers

Not I and Cloned

This sequence belongs to sequence cluster 497.f

Location/Oualifiers
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Full-1. Gruber C. Jessee, J. and Polayes, D. Unpublished (2001)

Unpublished (2001)
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/tissue_type="ADULT BRAIN"
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/clone_lib="idomo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSpORT 6; lst strand cDNA
enriched, double-strand cDNA was digested with not I and
vector. Library was not normalized " of the pCMVSpORT 6
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/mol_type="mRNA"
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/clone="CSODNOO3YLL19"
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On Feb 13
Contact:
                                                                                                                AL527972 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo cDNA clone CSODC027YP19 5-PRIME, mRNA sequence.
AL527972 AL527972 AL527972.3 GI:45703058
         Li, W.B., Gruber, C., Jessee, J. Full-length CDNA libraries and Unpublished (2001)
On Feb 13, 2001 this sequence
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 726)
                                                                                            Homo sapiens
                                                                                                      Homo sapiens (human)
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Pred. No. 2.7e-129;
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          version replaced gi:31065823
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             GAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAA
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Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: segref@genoscope.cns.fr Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and clonec into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODC027CH10QP1&c=497.f. Location/Qualifiers
GAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAA
                                                                           CTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGA
                                                                                                                                                                                             ATGAAGGTGTTCGTCTGCAGCGCCTCCACATCGCACTCCGGGGAGAAGCCCGGTCCCCACT
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/db_xref="taxon:9606"
/db xref="taxon:9606"
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/clone lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Pred. No. 8.6e-124;
18; Mismatches 25;
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Search completed: April 19, 2005, 21:57:07

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No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on:
Homo sapiens
                                                      25-MAR-2003
03-OCT-1995
                 Ligand; cell surface; tyrosine kinase receptor; tumorigenesis; immunogen
                                    Human hek-L
                                                                                 AAR71481;
                                                                                                AAR71481 standard; protein;
                                                                                                                                                                                                                                                                                 Pred. No. is the nu score greater than and is derived by a
                                                                                                                                                                                                                                      Score
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                                                                                                                                                                                                                                                                                                                    A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003bs:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   length: 0 length: 2000000000
                                                                                                                                                                                                                                                                                 is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                        100.0
100.0
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1207
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                                    protein.
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Listing first 1500
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AAG79439
ABP97190
ADN38812
ADQ21666
AAR82605
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                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                  SUMMARIES
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1413.163 Million cell updates/sec
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                                                                                                                                                                     Aar71481 Human hek
Aag79439 Breast/co
Abp97190 Tumour-as
Adn38812 Cancer/an
Adq21666 Human sof
Aar82605 Eph trans
                                                                                                                                                                                                                                     Description
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RESULT 2
AAG79439
ID AAG7
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AC AAG7
XX
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XX
DE Brea
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukaemia cells that express the hek antigen. Hek-L also binds the elk tyrosine kinase receptors. See also AAR71482. (Updated on 25-MAR-2003 to correct PN field.)
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30-AUG-1993;
03-DEC-1993;
09-MAY-1994;
  Breast/colon cancer associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 238 AA;
                                         25-OCT-2002
                                                                              AAG79439;
                                                                                                                   AAG79439 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 21; Page 36; 45pp; English.
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leukaemia cells.
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                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219;
                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                  61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          س
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAAAPLILLLLLVPVPLLLPQGPGGALGNRHAVYMNSSNQHLRREGYTVQVNVNDYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ85887.
                                                                                                                                                                                                                 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKR 219
                                                                                                                                                                                                                                                                                                                                                                              IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAAAPLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD
                                                                                                                                                                                                                                                                                                KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT
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93US-00114426.
93US-00161132.
94US-00240124.
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1. .19
/note= "signal peptide"
20. .238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding hek-L protein or its fusion products - useful or for carrying therapeutic and diagnostic compounds t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1207; DB 2; 100.0%; Pred. No. 1.8e-115; tive 0; Mismatches 0;
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The sequences given in ABA00086-92 represent sequences which have been comparises determining the invention for diagnosing cancer. These sequences may be colorrectal tissue sample, or in a breast tissue sample, or a first reactment and prognosis of the invention is useful for the diagnosis.

CC individual. The method of the invention is useful for the diagnosis, cancer and prognosis of breast and/or colorectal cancer. The invention is useful for the diagnosis, corresponding to the contract of the invention of the colorectal cancer. The invention prognosticating breast and/or colorectal cancer. Prior methods of diagnosing and inhibiting composition of problematic. The present methods of gene therapy using novel sequences and purpose limitless and more specific especially in the area of correcting prognostic factors. This sequence represents CHA4 which has the breast cancer modulating prognostic factors. This sequence represents CHA4 which has the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing cancer by determining the expression profile gene that encodes the CHA4 or CBK8 protein, useful for the treatment and prognosis of
                                  181 LPÓFTMGENVKINVLEDFEGENÞÓVEKLEKSISGTSEKR 219
                                                    181 LPOPTMGPNVKINVLEDFEGENPOVPKLEKSISGTSPKR 219
                                                                              121 KPŚEKFORYSAPSLGYBPHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-2000; 2000US-00733756.
08-DEC-2000; 2000US-00733757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-2001; 2001WO-US048368.
                                                                                                                                                                                                                                                                    atch 100.0%; Score 1207; DB 5; 2al Similarity 100.0%; Pred. No. 1.8e-115; 219; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breast; colon; cancer; diagnosis; colorectal; prognosis; gene therapy; CHA4; CBK8.
                                                                                                                                                                                                                 KFSEKFORYSAFSLGYEFHAGHEYYY1STFTHNLHWKCLRMKVFVCCASTSHSGEKFVFT 180
                                                                                                                                     ÍÝCÞHÝNISSGVGÞGAGÞGÞGGGAÐQÝVLÝMVSRNGÝRÍCNASQGÞKRWECNRÞHÁÐHSÞÍ 120
                                                                                                                                                          | IYCPHYNSGYGPGAGPGPGGAEQYYLYMYSRNGYRTCNASOGFKRWECNRPHAPHSPI 120
                                                                                                                                                                                              MAAAPLLLLLLVPVPLLPLLAQGPGGALGNRHAVYMNSSNQHLRRBGYTVQVNVNDYLD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
6. .238
/note= "Encoded by ABA00091"
                                                                                                                                                                                                                                                                                           Length 238;
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                                                                                                                                               Query Match
Best Local Simi
Matches 219;
                                                                                                                                                                                                ACC49493 to ACC49552 encode the human tumour-associated antigenic target (PMT) proteins given in ABP97175 to ABP97234. The present invention describes an isolated antibody that binds to a polypeptide having at sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking the associated signal peptide, encoded by any of the 60 2000-3000 hase cytostatic activity. The antibody can be used for treating or diagnosing cumours or cancers in mammals, e.g. prostate cancer, lung cancer, ovarian cancer, prostate adenocarcinomas, or thyroid cancer, prostate adenocarcinomas, renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-2001; 2001US-0323268P.
19-OCT-2001; 2001US-0339227P.
07-NOV-2001; 2001US-03396827P.
20-NOV-2001; 2001US-033969.
03-APR-2002; 2002US-0345444P.
19-AUG-2002; 2002US-0369724P.
19-AUG-2002; 2002US-0404809P.
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2, Fig 72; 285pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     New antibodies against tumor-associated antigenic target polypeptide, prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-354551/33.
N-PSDB; ACC49508.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frantz G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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                                                                            01-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP97190;
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ĨŶĊĔĦŶŇŚŚĠŶĠĒĠĀĠĒĠĠĠĀĒĠŶVĹŶĸŶŚŖŇĠŶŖŦĊŇĀŚĢĠĒĶŖŴĒĊŇŖ₽ĦĀĔĦŚŖĨ
                     IYCPHYNSSGYGPGAGPGGGAEQYVLYMYSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
                                                       MAAAPLLLLLLVPVPLLPLLAQGPGGALGNRHAVYMNSSNQHLRKBGYTVQVNVNDYLD
                                                                                                                                                          Similarity
                                                                                                                                     ilarity 100.0%; s
Conservative 0;
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PM, Wu TD, !
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                                                                                                                           Score 1207; DB 6;
Pred. No. 1.8e-115;
Mismatches 0;
                                                                                                                        Indels
                                                                                                                                                     Length
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Ś 8 Ş Дb Ş 뭐 Ś

121 KPSEKFORVSAFSIGYEFHAGHEYYYISTÞTHNÍHWKCLRMKVFVCCASTSHSGEKÞVÞT 121 KFSEKFORYSAFSLGYEFHAGHEYYYISTETHNIHMKCIRMKVFVCCASTSHSGEKFVPT 180

180

121

61

13

Matches Query Match Best Local

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RESULT 4
ADN38112
ID ADN3812
XX ADN3812
XX ADN3812
XX ADN3812
XX ADN3
XX C ADN3
XX C ADN3
XX C CANC
XX Human
XX W Fibir
XX W Vulit
XX W Vulit
XX W Vulit
XX V Vulit
XX V Vulit
XX PPU 22-i
XX Z 2-i
PR 13-
XX Z 2-i
PR 13-
XX Z 13-
PR 113-
XX Z 13-
PR 21-
PR 22-
PR 2
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21-NOV-2001;
29-NOV-2001;
03-DEC-2001;
14-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002;
20-FEB-2002;
29-MAR-2002;
04-APR-2002;
12-APR-2002;
05-JUN-2002;
16-JUL-2002;
The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising invention also relates to expression vectors and host cells comprising onlypeptide of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JAN-2002;
10-JAN-2002;
                                                                                                                                                                                                                                                                                                                             Determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory disease; autoimmune disease;
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                                                                                                                                                                                                                                                                                    nucleic
                                                                                                                                                                                                                                                                                                                                                                              2003-468649/44.
DB; ADN38811.
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                                                                                                                                                                                                                                                                                                          for
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Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder; psoriasis; ischaemia; heart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-0332464P.
2001US-033433P.
2001US-0335394P.
2001US-0340376P.
2002US-0347341P.
2002US-0355250P.
2002US-035590774.
2002US-03590779.
2002US-036809P.
2002US-0370110P.
2002US-0370110P.
2002US-037014P.
2002US-0396614P.
2002US-0397845P.
2002US-0397845P.
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                                                                                                                                                                                                                                   1385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   T WM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; angiogenic disorder;
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E, Zlotnik
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and methods of screening for modulators of activity or expression polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and transpositions and methods such as psoriasis, ischaemia, heart di atherosclerosis, inflammatory diseases, autoimmune diseases, retin neovascularistaion syndromes, scarring and uterine fibroids. They also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.
                                                                                                                Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                        Aziz N,
                                                                                                                                                                                                                                       26-NOV-2002; 2002US-0429739P
                                                                                                                                                                                                                                                                                       10-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                             soft tissue sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                     Human soft
                                                                                                                                                                                                                                                                                                                                                                                                            26-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                             cytostatic; gene therapy; vaccine; screening;
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Pred. No. 1.8e-115;
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which comprises obtaining a first soft tissue sample from a and a normal soft tissue sample from the same or different determining the expression of a gene in both samples and co expression of the gene in both soft tissue samples, where a of protein expression in the first soft tissue sample indic

Example

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method for detecting soft tissue sarcomat soft tissue sample from an individual

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WPI; 1995-358635/46.
N-PSDB; AAT03883.
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AAR82605
ID AAR8
                                                                                                                                                       04-APR-1994;
12-APR-1994;
01-SEP-1994;
21-OCT-1994;
                                                        Davis S, Gale N,
Yancopoulos GD;
                                                                                                   (REGE-) REGENERON PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Efl-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand;
neurological disorder; identification; diagnosis.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR82605 standard; protein; 234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic fine current sequence is that of a human soft tissue sarcoma-uprogulated protein of the invention. The current sequence is that of a human soft tissue sarcoma-uprogulated specification per se but was submitted in CD format by the inventor.
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al Similarity 100.0%; Score 1207; DB 8; Length 238;
219; Conservative 0; Mismatches 0; Indels 0
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94US-00299567.
94US-00327423.
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                                                            Aldrich TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 note= "residue borders main conserved regions"
                                                                                                                                                                                                                                                                                                                                    "carboxy terminal hydrophobic GPI-recognition
                                               Maisonpierre PC,
                                    Goldfarb M;
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Search completed: April 19, 2005, 23:13:33
Job time : 59.9368 secs
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.2
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Ef1-2 (also known as EHK-1L) is an Eph transmembrane tyrosine kinase ends in a C-terminal hydrophobic sequence that appears to to be intracellular domain. Ef1-2 is useful for identifying other ligands for a differential function and/or influence that appears to to be a Ehk-1, -2, -3, Eck and Elk receptors. The ligands are useful in an and/or proliferation, of receptor bearing the phenotye, such as growth diagnosis, and treatment of neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ligands which bind Eph family receptors - used in the diagnosis of
                                                  177 LPQFTMGPNVKLNVLEDFEGENPQVPKLEKSÍSGTSPKR 215
                                                                             181 LPQFTWGPNVKINVLÄDFEGENPQVPKLEKSISGTSPKR 219
                                                                                                      117 kŕsekrorysarsláverhághevyvístprhníhnkolknikvevocástshágekropt 176
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                                                                                                                               KESEKFORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
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98.2%; Pred. No. 7.2e-112;
tive 0; Mismatches 0;
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Human hek-L protein cDNA clone

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Minimum
Maximum
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.		Match	Match Length DB	BB	ID	Description
₽ .		100.0	- 1	2	AAQ85888	Aaq85888 Human hek
N	546	100.0		œ	ABZ34863	Abz34863 Coding se
w	544.4	99.7		σ	ABV78135	Abv78135 Human eph
4	544.4	99.7		σ	ABZ35711	Abz35711 Human eph
₅	544.4	99.7	606	σ	ABX09954	Abx09954 Human eph
6	544.4	99.7		Q	ABL91676	Abl91676 Human pol

ALIGNMENTS

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RESULT 1
AAQ85888
ID AAQ8
XX
AC AAQ8
XX
DT 25-N
DT 03-C
XX
        25-MAR-2003
03-OCT-1995
                                              AAQ85888
                                              standard;
       (revised)
(first entry)
                                              CDNA
                                              ç
                                             mRNA;
                                              636
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В S 밁 S 멼 Ś 밁 8 Query Match Best Local Similarity Matches 546; Conserva The sequence is that of a clone encoding hek-L protein, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukaemia cells that express the hek antigen. Hek-L also binds the elk tyrosine kinase receptors. See also AAQ85887. (Updated on 25-MAR-2003 to correct PN field.) 20-AUG-1993; 30-AUG-1993; 03-DEC-1993; 09-MAY-1994; Cbs Sequence 636 BP; 102 A; 202 C; 186 G; 146 T; 86 .88 Claim 3; Page 37; 45pp; English. New isolated DNA P-PSDB; AAR71482. WPI; 1995-106811/14. Beckmann MP, mat_peptide sig_peptide Ligand; leukaemia cells. (IMMV) IMMUNEX CORP. 17-AUG-1994; 02-MAR-1995. WO9506065-A1 Homo assay reagent 121 241 208 181 148 sapiens 88 13 28 cell CCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCC TACGAAGGCCCAGGGCCCCCTGAGGGCCCCCGAGACGTTTGCTTTGTACATGGTGGACTGG CGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCAC CGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAACCCCAGGTTGCTT ATGCGGCTGCTGCCCCTGCGGACTGTCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTG TACGAAGGCCCAGGGCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGG CGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCCAC ATGCGGCTGCTGCCGCTGCGGACTGTCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTG Conservative surface; tyrosine kinase receptor; tumorigenesis; Cerretti 93US-00109745. 93US-00114426. 93US-00161132. 94US-00240124. 94WO-US009282 /*tag= k 94. .630 /*tag= c /*tag= 28. .93 28. Location/Qualifiers encoding hek-L protein or its fusion products - useful or for carrying therapeutic and diagnostic compounds to 28. .633 100.0%; Score 546; DB 2; 100.0%; Pred. No. 2.1e-138; DP; ۵ 0; Mismatches 0 U; 0 Other; Length 636; Indels 0; immunogen; Gaps 300 207 180 267 240 147 120 87 0

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Query Match

Best Local Similarity 100.0%; Score 546; DB 8; I

Matches 546; Conservative 0; Mismatches 0;
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ABZ34863
ID ABZ3
                                                                                                                                         The present invention relates to novel nucleotide sequences, which are differentially expressed in models of osteogenesis upon being put in contact with a stimulator of osteogenesis. The present sequence is one such sequence. This sequence can be used for diagnosing osteoporosis/bone disease in a pattent, promoting osteogenesis and/or preventing osteoporosis/bone disease. The present sequence encodes a Ephin-ephrin family protein
                                                                                                        Sequence 1181 BP; 234 A; 353 C; 331 G; 263 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid upregulated/downregulated in osteogenesis, useful for bone disease therapy in subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Garcia T, Ro
                                                                                                                                                                                                                                                                                                  Claim 1; Page 214; 237pp; English.
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26-OCT-2001; 2001DE-01055280.
29-NOV-2001; 2001DE-01058411.
07-DEC-2001; 2001DE-01060151.
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Best Local (
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target and
 07-FEB-2003
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                                                             standard;
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   (first entry)
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                                                            DNA;
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.5e-138;
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Human ephrin A3 encoding polynucleotide SEQ Ħ Ö 19

protozoacide; gene expression; antisense; tumour; infection; Plasm virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds. Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide; infection; Plasmodium Plasmodium;

18-JUL-2002.

09-JAN-2001; 2001DE-01000588

09-JAN-2001; 2001DE-01000588

(RIBO-) RIBOPHARMA న ద

Kreutzer æ Limmer ŝ Rost ß Hadwiger

2002-683450/74.

Inhibiting expression by introducing into ce to the target. on of target genes, useful cells two double-stranded e.g. for treating that are comp complementary

Claim 13; Page 19-20; 100pp; German.

The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (dsnNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each of dsnNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAi). The method is particularly used to treat tumours or infections, especially by plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the invention

Sequence 606 BP; 96 A; 191 C; 175 G; 144 T; 0 **;** 0 Other;

Query Match Best Local

Similarity

99.7%;

Score 544.4; Pred. No. 5.5

Indels Length

0

Gaps

0

밁 S 밁 S 맑 S 밁 δ 밁 S Matches 301 181 181 241 121 121 545; 61 61 CTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCCTC CCAGGCTATGAGTCCTGCCAGGCAGAGGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCC CGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCCAC CGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAACCCCAGGTTGCTT ATGCGGCTGCTGCTGCTGCGGACTGTCCTCTGGGCCGCTTCCTCTGGCTCCCCTCTG TACGAAGGCCCAGGGCCCCCTGAGGGCCCCCGAGACGTTTGCTTTGTACATGGTGGACTGG CCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCC TACGAAGGCCCAGGGCCCCTGAGGGCCCCCGAGACGTTTGCTTTGTACATGGTGGACTGG CGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCAC CGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAACCCCCAGGTTGCTT Conservative 0, Mismatches 1; DB 6; 5.5e-138; hes 1; 180 300 300 240 240 120 360 180 120 60

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This invention describes a novel method for inhibiting expression of a crayet gene by introducing into the cell that contains the target gene at least one oligoribonucleotide (dsrNAI) that has a double-stranded (ds) created a segment of one strand of the ds tructure is complementary with the target gene and the cells are treated with interferon before target genes, particularly oncogenes, cytokine genes, id (not defined) to used to inhibit expression of CC protein genes; developmental or prion genes, or genes expressed in the target genes, alimals or plants). Treating the cells with cc expression of the target genes, and the effect is even greater when dsrNAI creates their stability. ABX0993-ABX10075 represent or minimals used to illustrate the method of the invention
                 Query Match
                                                                                                                                                                                                                                             Disclosure; Page 24-25; 98pp; German.
                                                                                                                                                                                                                                                       Inhibiting expression of target genes, e.g. oncogenes, in cells, by treating the cell with interferon.
                                                                                                                                                                                                                                                                                                                                                                          (RIBO-) RIBOPHARMA AG.
                                                                                                                                                                                                                                                                                                                                                                                              09-JAN-2001; 2001DE-01000587.
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                  606 BP; 96 A; 191 C; 175 G; 144 T; 0 U; 0 Other;
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Score 544.4; DB 6;
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WPI; 2002-270454/32
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Matches 545; Conservative
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Query Match
Best Local Similarity
Matches 545; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 606 BP; 96 A; 191 C; 175 G; 144 T; 0 U; 0 Other;
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Pred. No. 5.5e-138;
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Search completed: April 19, 2005, 16:26:10 Job time: 391.513 secs

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                                                                                                                                                                                                                                            RESULT 1
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                                                                                                                                                                                               Sequence 3, Application US/08240124 Patent No. 5516658
                                                                      APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT I
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
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Maximum Match 100%
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CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK
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FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
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NAME/KEY:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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CURRENT APPLICATION DATA:
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CLONE: hek-L C6
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COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOPTWARE: Microsoft Word for Apple
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STRANDEDNESS: single
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TELEFAX: (206) 233-0644
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                                CCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCC
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                                                                                                                                                                                                                                                                                                                                                                         Score 546; DB 1;
Pred. No. 1.9e-142;
                                                                                                                                                                                                                                                                                                                                                            Mismatches
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RESULT 2 US-08-453-943-3

568 CCCÁGC 573

541

CCCAGC 546

В Ś В Ş В Ş

481 508

448

421

361 328

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COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/453,943
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/453,943
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/161,132
APPLICATION NUMBER: US/08/114,426
APPLICATION NUMBER:
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Patent No. 5738844
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERESTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE;
NUMBER OF SEQUENCES:
ADDRESS:
ADDRESS:
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STATE: SEATTLE
STATE: WASHITT
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Patent No. 5969110

GENERAL INFORMATION:
APPLICANT: BECKNANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
INUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ANDERSCEP. TMAINTEN CORDORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-057-121-3
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ADDRESSEE: IMMUNEX CORPORATION STREET: 51 UNIVERSITY STREET CITY: SEATTLE
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Best Local S
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LOCATION: 94.630
FEATURE:
NAME/KEY: CDS
LOCATION: 28.633
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE
CLONE:
FEATURE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 ccáddetardágrectráccáddádádáddececciddagectrácáddececradardráctce 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TACGAAGGCCCAGGGCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 ČĠĀĠĠĀĠĀĊĠĊĠŦĠĠŦĠĠĀĠĊŤĠĠĠĊĊŤĊĀĀĊĠĀŤŤĀĊĊŤĀĠĀĊĀŤŤĠŤĊŤĠĊĊĊĊĀĊ 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĠĊĊĊŔŦĊĊŦĠŤŢĠĠĠŔĠĊĊĊŦĠĠŔĠŔĠŔĠŔĠŢĠĠĊŔĊŔŢĊŔĠĠĠŦĠĠĊĠŔĠĠĠĠĠĠĠŔĊŔĊŢ
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9810

WASHINGTON

USA

TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 3

SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: CDNA to mRN/

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TELEPHONE: (206) 233-0644

HYPOTHETICAL:

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CDNA to mRNA



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В
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                                                                                                                                                                                                                                                                         Query Match
Best Local :
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NAME: SEESE, KATHKEN A.

REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (206) 587-0430
TELECOMMUNICATION: (206) 587-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
FILING DATE:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple disk
COMPUTER: Apple System 7.1
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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CLONE: hek-L C6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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TELEFAX: 756822
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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                    181 TACGAAGGCCCAGGGCCCCCTGAGGGCCCCCGAGACGTTTGCTTTGTACATGGTGGACTGG 240
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                                                                                                                                                  CGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAACCCCCAGGTTGCTT
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100.0%; Pred. No. 1.9e-142;
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RESULT 4
US-09-358-734-3
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Patent No. 6274117
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APPLICANT: BECKWANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Apple System 7.1 SOFTWARE: Microsoft Word for Apple, CURRENT APPLICATION DATA:
                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION UMBER: US 08/109,745
FILING DATE: 20-AUG-1993
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MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Sy
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PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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STRANDEDNESS:
           LENGTH: 636 base pairs
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51 UNIVERSITY STREET
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linear CDNA to

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Sequence 1291, Application US/09949016
PATENT NO. 681233
GENERAL INFORMATION:
APPLICANT: VENTER, J. CTaig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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US-09-949-016-1291
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Best Local Similarity 100.0%; Score 546; DB 3; L
Matches 546; Conservative 0; Mismatches 0;
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CLONE: hek-L C6
FEATURE:
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LOCATION:
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Transcriptome characterization elucidates signaling networks control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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Location/Qualifiers
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/note="oligo dT primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem
line"
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Pred. No. 1.3e-129;
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Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Lebkowski, J and Stanton, L.W. Rao, M.S., Mandalam, R., Control, human ES cell growth and differentiation networks that Biotechnol. 22 (6), 707-716 (2004)

Regenerative Medicine

Butheria; Butheria, Character R. Torontollam, R., S., Mandalam, R., Controllam, R., Controll
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230 Constitution Drive, Menlo Park, CA 94025, USA
Fax: 650 473 7760
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17000600021389 GRN_PREHEP HOMO Sapiens CDNA 5', mRNA Sequence.
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/note="oligo dT_primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 1.3
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Tissue procurement: DcTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
here.//image 11m1 com.
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plate: LLCM2662 row: k column: 24
High quality sequence stop: 635.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="carcinoma, cell line"
/clone_lib="MH108 (phage-resistant)"
/clone_lib="MH108 (phage-resistant)"
/clone_lib="NH1 MGC 40" rector: porms, site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5 adaptor: GGRACGAG (G). Library constructed by
Cloned into EcoRI XhoI sites using the
of California, Berkeley) using ZAP-cDNA synthesis kit
Note: this is a NH_MGC Library."

(Stratagene) and Superscript II RT (Life Technologies).
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.7%; Score 544.4; DB 5;
99.8%; Pred. No. 1.4e-129;
tive 0; Mismatches 1;
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FEATURES SOUYCE	AUTHORS TITLE JOURNAL COMMENT	SOURCE ORGANISM REFERENCE	RESULT 4 CA454936 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Db Qy	Db Q	Db Qq	Qy	Db Qy	Qy Db	D Qy	Db
Tissue Procurement: Kristi A. Egland, Ira Pastan CDNA Library Preparation: Invitrogen Corp cDNA Library Preparation: Invitrogen Corp cDNA Library Preparation: Invitrogen Corp cDNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LiLAM14285 row: b column: 24 High quality sequence stop: 473. Location/Qualifiers 1. 898 e /organism="Homo sapiens" //ob_xref="raxon:9606" //clone="IMAGE:6722424" //clone="IMAGE:6722424" //clone="IMAGE:6722424" //clone lib="MAPCL" //note="Vector: pCMV-SPORT6; SK-BR-3, MDA-MB-231, Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg,	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Fmail. Cranberremail nih Gov		CA454936 AGENCOURT_10714679 MAPCL Homo sapiens cDNA clone IMAGE:6722424 5', mRNA sequence. CA454936 CA454936.1 GI:24905152	541 CCCAGC 546 596 CCCAGC 601	481 GCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGCACATCAGGGTGGCGAGGGGGGGACACT 540	421 TCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGGAGAGGAAGTCTGAGTCA 480	361 GGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGT 420	301 CTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTC 360	241 CCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCC 300 [181 TACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGG 240	176 CGAGGÁGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCAC 235
RESULT 5 BE883793 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	B &	Q Q	OY OY	\$ \$ \$				}	Query Best Match	ORIGIN	
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ilarity 98.9%;
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Pred. No. 1.1e-127;
0; Mismatches 6;
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karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 707)
H-MGC http://mgc.nci.nih.gov/.
tional Institutes of Health, Mammalian Gene Collection (MGC)
published (1999)
ntact: Robert Strausberg, Ph.D.
ail: Cgapbs-r@mail.nlh.gov
ssue Procurement: ATCC
DNA Library Preparation: Life Technologies, Inc.
DNA Library Preparation: The Technologies, Inc.
NA Sequencing by: Tneyte Genomics, Inc.
NA Sequencing by: Noyte Genomics, Inc.
NA Sequencing by: Moyte Genomics, Inc.
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BI868252 GI:16041925
Homo sapiens (human)
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Plate: LLAM971E row: b column: 23
High quality sequence stop: 706.
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j. .707
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/mol_type="mRNA"
/db_xxef="taxon:9806"
/db_xxef="taxon:9806"
/clone="JMAGE:3907510"
/tissue_type="leiomyosarcoma"
/lab_host="NHHGE:3907510"
/clone_lib="NHHMGC:71"
/note="Organ: uterus, Vector: pCMV-SpORT6; Site_1: NotI;
Site_2: SalI; Cloned unddirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
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99.6%; Pred. No. 1.6e-126;
ative 0; Mismatches 1; Indels 1;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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                                                                                                                                                                                                                                                                                              CGCGGGGGCTCCAGCCTCCGCCACGTAGTCTGCAACTCCAGTAACCCCCAGGTTGCTT 120
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CTGCCCTTTGGCCATGTTCAATTCTCAAGAGAAGATTCAGCGCTTCACACCTTTTCTCCCCTC
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                                                         CCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCC
                                                                                  CCAGGCTATGAGTCCTGCCAGGCAGAGGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCC 300
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/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo c Average insert size 2 kb. Library constructed by Life Technologies."
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/cissue_type="melanotic melanoma"
/lab_hogi="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_72"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 1.2e-123;
); Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                  Geron Corporation
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Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,I
Lebkowski,J and Stanton,L.W.
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Brandenberger,R., Wei,H., Zhang,S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CN289864
                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 650 473 8658
Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 Constitution Drive,
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                                                                                                                                                                                 Similarity
 ATTGTCTGCCCCCACTACGAAGGCCCCAGGGCCCCCTGAGGGCCCCCGAGACGTTTGCTTTG
                 ATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCCGAGACGTTTGCTTTG
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/note="Oligo dT_primed, ful
from undifferentiated hES c
and H9 (p26) maintained in
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                              91.5%;
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                                                                                                                                                                 Score 499.4; DB 7;
Pred. No. 5.3e-118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.min.gov

CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from piero carninoi (RIKEN)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: McC clone distribution information can be

http://image.llnl.gov

Plate: NDAM34 row: O column: 10

By Agencourt Bloscience Corporation

http://image.llnl.gov

Location/Oualifiers

High quality sequence stop: 514.

Location/Qualifiers
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1 (bases 1 to 834)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.
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MSENCOURT 13666148 NIH MGC 148 Homo Sapiens cDNA clone
CB996846.
                                                                                 /tissue_type="pre-eclamptic placenta"
/lab host="pre-eclamptic placenta"
/clone lib="NIH MGC 148"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
directionally cloned using primer
size_2: BanH; Library is oligo-dT primed and
size_1: placenta; Vector: pBluescriptR; Site_1:
directionally cloned using primer
size_2: BanH; Library is oligo-dT primed and
size_2: Ab and normalized to ROT 5. This is a primary
library enriched for full-lenght clones and constructed
using the Cap-trapper method (Carninci, in preparation)
Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30332601"
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Best Local S
Matches 528
                                                                                                                  Homo sapions
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 592)
Wistow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal, A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.,
Expressed sequence tag analysis of adult human iris for the NEIBank
Mol. Vis. 8 (4), 185-195 (2002)
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethaeda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            639 ĆAĆ 641
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S92 bp mRNA linear EST 24-JUN-2003 CD671399 GRIVA Sequence.
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Pred. No. 1.1e-117;
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Plate: 04 row: c column: 02
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                      TACGAAGGCCCAGGGCCCCCTGAGGGCCCCCGAGACGTTTGCTTTGTACATGGTGGACTGG 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="Human Iris cDNA (Normalized): fg"
/note="Organ: Eye; Vector: pcMVSPORT6; A human iris
library (bx) was normalized by self-sertion. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
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dev_stage="Adult"
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Search completed: April 19, 2005, 21:57:12 Job time : 2540.83 secs

Wilson What Is John Sill

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Result
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Sequence 4, Application US/09904954 Patent No. US20020010325A1 GENERAL INFORMATION:
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                 Length DB
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_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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7 US-10-698-907-12
3 US-10-138-787-8
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                                                                                                                                            ALIGNMENTS
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Million cell updates/sec
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Sequence 12, Appl
Sequence 8, Appli
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Best Local S
Matches 179
                                                                                                                                     Sequence 12, Application US/10698907
Publication No. US20050049194A1
GENERAL INFORMATION:
                 APPLICANT: Frisen, Jonas
APPLICANT: Holmberg, Johan
TITLE OP INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
TITLE OP INVENTION: Proliferation
FILE REFERENCE: 21882-529 UTIL
CURRENT APPLICATION NUMBER: US/10/698,907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/904,954
FILING DATE: 12-Jul-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION NUMBER: U8/240,124
FILING DATE: CUNKnown>
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
APPLICATION NUMBER: US 08/109,745
FILING DATE: 10-AUG-1993
AFFORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BECKMANN, M. P.

CERRETTI, DOUGLAS P.

TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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179; Conserv
                                                                                                                                                                                                                                                                                                        121 GFEFÉPGETYYYISVÉTFESSGÓCLRÉGVSVCCKERKSESAHPVGSPGESGTSGWRGGD 179
                                                                                                                                                                                                                                                                                                                                   121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGD 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRLLPILRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                                                                                                                                                                                                      YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 989; DB 9; 100.0%; Pred. No. 2.4e-96; tive 0; Mismatches 0;
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Sequence 8, Application US/10138787

Publication No. US20020172984A1

Publication No. US20020172984A1

APPLICANT: Holland, Sacha
APPLICANT: Holland, Sacha
APPLICANT: Holland, Sacha
APPLICANT: Mosmalu, Geraldine
TITLE OF INVENTION: DIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR

CURRENT APPLICATION NUMBER: US/10/138,787

PRIOR APPLICATION NUMBER: US/09/214,631

PRIOR APPLICATION NUMBER: US/09/214,631

PRIOR APPLICATION NUMBER: US/09/214,631

PRIOR APPLICATION NUMBER: US/09/214,631

PRIOR APPLICATION NUMBER: DOT/05/00473

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/021,272

NUMBER: DATE: 1996-07-05

SOPTWARE: Patentin User 2 0

SOPTWARE: Patentin User 2 0
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                                                                                                                                                                                                                                                                                  LENGTH: 201

TYPE: PRT

ORGANISM: Homo sapiens
US-10-138-787-8
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PRIOR APPLICATION NUMBER: US 60/460,488
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US 10/291,290
PRIOR PILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR PRILING DATE: 2002-07-02
PRIOR PILING DATE: 2002-07-02
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
SOFTWARE: PatentIn NOS: 25
SOFTWARE: PatentIn Version 3.2
LENGTH: 201
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                    Query Match

98.2*; Score 971; DB 13; Length 201;

Best Local Similarity 98.3*; Pred. No. 1.9e-94;

Matches 176; Conservative 0; Mismatches 3; Indels
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100.0%; Score 989; DB 17;
Best Local Similarity 100.0%; Pred. No. 2.4e-96;
Matches 179; Conservative 0; Mismatches 0;
61 YEGÞGÞÞEGÞETÞÁLYMYDWÞGYESCQÁÉGÞRGYKRWVCSLÞÞGHVQÞSEKÍQRÞTÞÞSL 120
                                                                             121 GPEFLPGETYYYISVPTPESSGOCLRLOVSVCCKERKSESAHPVGSPGESGTSGWRGGD 179
                             YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
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121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGD 179
                   121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGD 179
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Search completed: April 19, 2005, 23:22:25 Job time : 35.3289 secs

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                          US-08-240-124-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
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                                                                                                                                                                                                   Sequence 4, Applic Patent No. 5516658
                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGI
                                                                                                        APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT
TITLE OF INVENTION: RECEPTOR HEK
                                                                     CORRESPONDENCE ADDRESS:
                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                  STREET:
                                                      ADDRESSEE:
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                 SEATTLE
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WASHINGTON
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Match
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100.0
100.0
100.0
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                                  51 UNIVERSITY
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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/EB_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*
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Maximum Match 100%
Listing first 1500 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyright
                                                      IMMUNEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                    CORPORATION
ITY STREET
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US-08-453-943-4

US-09-057-121-4

US-09-358-734-4

US-09-349-016-7162
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                                                                                                                             BINDS THE CELL
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Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 7162, Ap
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US-08-453-943-4
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                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08453943 Patent No. 5738844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 989; DB 1; Best Local Similarity 100.0%; Pred. No. 2.6e-107; Matches 179; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/240,124
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Sys
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                   ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OFERALING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version
CURRENT APPLICATION DATA:
APPLICATION ATTAIN
                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: INVINEX CORPORATION
STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                       APPLICANT: BECKMANN, M. APPLICANT: CERRETTI, DO TITLE OF INVENTION: CYTTITLE OF INVENTION: REC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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TELEFAX: 756822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 28
  COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple S
                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                    SEATTLE WASHINGTON
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CYTOKINE THAT I
RECEPTOR HEK
Apple System 7.1
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                                                                                                                                                                                                                                                             BINDS
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                                                                                                                                                                                                                                                             CELL SURFACE
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CLASSIFICATION: 530 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132

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APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GPÉFLÉGETYYYİSVÉTÉÉSSGQCLRLQVSVCCKERKSESAHEVGSÉGÉSGÉSGMRGGÉ 179
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RRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRLLELLRTYLWAAPLGSELRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCEH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YBÓÞÓÞÞÉGÞÉTÞALYNVDWÞÓYESCOÁÞÓÞRÁYKRWVCSLÞFGHVOFSŠÉKÍÐRÞTÞÞSL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 201;
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                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acids
TOPE: Information acids
TOPE: Tree: Thear
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APPLICANT: CERRETTI, DOUGLA,
TITLE OF INVENTION: CYTOKIN,
TITLE OF INVENTION: RECEPTO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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Stent No. 6274117
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ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
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Best Local Similarity
                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                    COUNTRY:
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NAME: $20-AUG-1993
NAME
APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ĠŕĖŕĹÞĠĖTYYYÌŚVÞŤÞÉŚŚGŎĊĹĸĹŌVŠVĊĊKĖŔKŚĖŚĀHĒVĠSPĞĒŚĠŤŚĠWŔĠĠĎ 179
                                                                                                                                                                                                                                                                                               SEATTLE WASHINGTON
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CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              98101
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                                                                                                                                                                                                                                                                               USA
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CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK
                                                          US/09/358,734
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100.0%; Pred. No. 2.6e-107; I
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SR: 2814-C
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US-08-453-943-4

MOLECULE TYPE: protein

TOPOLOGY :

amino acids

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 201 amino acids

4:

PRIOR DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
PILING DATE: 20-AUG-193
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
12,172

APPLICATION NUMBER: FILING DATE: 30-AU

APPLICATION DATA:

03-DEC-1993

ATTUKNES, ASSESS KATTHKYN A. REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
0,06) 587-0440

2814-C

Query Match Best Local Similarity 100. Matches 179; Conservative

100.0%; Score 989; DB 1; I 100.0%; Pred. No. 2.6e-107; tive 0; Mismatches 0;

Sequence 4, Application US/09057121 atent No. 5969110 GENERAL INFORMATION:

CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION

F: 51 UNIVERSITY STREET
SEATTLE
WASHINGTON

USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple S

RE: Microsoft Word for Apple
APPLICATION DATA:
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ATION NUMBER

Word for Apple, Version 5.1a

US/09/057,121

08/240,124

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US-09-949-016-7162
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                                                                        Best Loc
Matches
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SEQ ID NO 7162
LENGTH: 210
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7162, Application US/09949016 Patent No. 6812339
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Best Local Similarity
                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 2814
REFERENCE/DOCKET NUMBER: 2814
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
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FILING DATE:
PRIOR APPLICATION DATA:
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TELEFAX: 756822
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                    MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
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MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH
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                                                                    100.0%; ilarity 100.0%; Conservative 0,
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Pred. No. 2.6e-107;
D; Mismatches 0;
                                                                                     Score 989; DB 4; Length 210; Pred. No. 2.8e-107;
                                                                      Mismatches
                                                                      <u>,</u>
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OF DETECTION AND
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US-09-214-631-8
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EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                        Query Match 98.2%;
Best Local Similarity 98.3%;
Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR TITLE OF INVENTION: TYROSINE KINASES FILE REFERENCE: 11757.23USWO CURRENT FILLING DATE: 1999-03-12 EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
EARLIER FILING DATE: 1997-07-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mbamalu, Gera
APPLICANT: Pawson, Tony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Holland, Sacha
                                                                                                                                                                                                                                                                                                                                                          LENGTH: 201
TYPE: PRT
ORGANISM: Homo sapiens
121
                          121 GPEFLPGETYYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGD 179
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                                                                                                          YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
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GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGD
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Pred. No. 3.3e-105;
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Search completed: April 19, 2005, Job time : 14.1316 secs 23:19:49

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03-OCT-1995
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                                                                      Peptide
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/note= "signal peptide"
23. 201
                                                                                                     Location/Qualifiers
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Matches 179
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03-DEC-1993;
09-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytocoxic agents to particular leukaemia cells that express the hek antigen. Hek-L also binds the elk tyrosine kinase receptors. See also AAR71481. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                 Sequence 201 AA;
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N-PSDB; AAQ85888.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as assay reagent
leukaemia cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated DNA encoding hek-L protein or its fusion products - useful as assay reagent or for carrying therapeutic and diagnostic compounds t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beckmann MP,
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                                                                                                                                   YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
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93US-00114426.
93US-00161132.
94US-00240124.
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Listing first 1500
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ABL91676
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                                                                                                                                                                       ADN02769
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                                                                                                                               ALIGNMENTS
                                                                 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (without alignments)
8258.620 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGGGGGGACACTCCCAGC
                                                                                                                                                                   Aaq85888 Human hek
Abz34863 Coding se
Abv78135 Human eph
Abz35711 Human eph
Abz0954 Human eph
Ab191676 Human pol
Adn02769 Human rec
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Best Local S
Matches 480
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03-DEC-1993;
09-MAY-1994;
                                                                                                                                                                                                                                                                                 The sequence is that of a clone encoding hek-L protein, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukaemia cells that express the hek antigen. Hek-L also binds the elk tyrosine kinase receptors. See also AAQ85887. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated DNA encoding hek-L protein or its fusion products - useful as assay reagent or for carrying therapeutic and diagnostic compounds to leukaemia cells.
                                                                                                                                                                                                                                                 Sequence 636 BP; 102 A; 202 C;
                                                                                                                                                                                                                                                                         correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 37; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beckmann MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-106811/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9506065-A1.
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274
                                                                                              154 GACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCACTACGAA
                                                                                                                                                                                                 480;
                                                                                                                      61
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                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR71482
                                                            GGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGC
                                                                                                             GACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCCACTACGAA
                                                                                                                                                               GGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGGTAACCCCCAGGTTGCTTCGAGGA 60
                      TATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCC 240
                                                                                                                                                GGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAACCCCCAGGTTGCTTCGAGGA
                                                                                                                                                                                                 Conservative
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93US-00114426.
93US-00161132.
94US-00240124.
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28..93
/*tag= b
94..630
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 28. .633
                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone
                                                                                                                                                                                                 0;
                                                                                                                                                                                                           Score 480; DB 2;
Pred. No. 2.2e-129;
                                                                                                                                                                                                                                                 186 G; 146 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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514

421

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The present invention relates to novel nucleotide sequences, which are differentially expressed in models of osteogenesis upon being put in such sequence. This sequence can be used for diagnosing osteoperce is one osteopercesis/bone disease in a patient, promoting osteopercesis and/or preventing osteopercesis/bone disease. The present sequence encodes a Ephin-ephrin
                                                                                                                                                                                                          Sequence 1181 BP;
                                                                                                                                                                                                                                                                                                           Claim 1; Page 214; 237pp; English.
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-058567/05.
                                                                                                                                                                                                                                                                                                                                                                                                                           (AVET ) AVENTIS PHARMA SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2001; 2001US-0281400P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2002; 2002WO-IB002211.
                                                 154 GÁCGCCGTGGTGGÁGCTGGGGCCTCAÁCGÁTTÁCCTÁGÁCÁTTGTCTGCCCCCÁCTÁCGÁ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W0200281745-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Osteopathic; osteogenesis modulator; gene therapy; osteogenesis; osteoporosis; bone disease; upregulator; human; ephin-ephrin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coding sequence SEQ ID 221,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABZ34863 standard; cDNA; 1181
                                                                                                                                                                                                                                                                                                               isolated nucleic acid upregulated/downregulated in osteogenesis,
                                                              GACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCACTACGAA 120
                                                                                                                                                                        Similarity
                                                                                         ddetrechdeetreedeethaeterhetrogaalereehdraheetekaetrieetredada 153
                                                                                                       GGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGA 60
                                                                                                                                                            Conservative
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, Jackson A, F
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                                                                                                                                              100.0%; Score 480; DB 8; L
100.0%; Pred. No. 2.7e-129;
n. Mismatches 0;
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Bushnell SE,
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                                                                                                                                                                                                                                                                                                                                                                                  Call K,
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                                       The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded (as1) of dsRNA1 is complementary to (I) and at least part of one strand has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA1 greatly increases effectiveness for inhibiting gene expression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
ABV78135
                                                                                                                              Claim 10; Page 123; 203pp; German.
                                                                                                                                    Inhibiting expression of target gene, useful e.g. for inhibiting concogenes, by administering double-stranded RNA complementary to
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26-OCT-2001; 2001DE-01055280.
29-NOV-2001; 2001DE-01058411.
07-DEC-2001; 2001DE-01060151.
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                                                                                                                                                                                                                                                                                                                                                                                     RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic; virucide; protozoacide; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ephrin-A3 DNA SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2002 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABV78135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABV78135 standard; DNA;
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Best Local
                                                                                                                                                                                 Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide; protozoacide; gene expression; antisense; tumour; infection; Plasmodium virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
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                                                                                                                                                                                                                                                                                                                ABZ35711 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of
 WPI; 2002-683450/74
                     Kreutzer R,
                                                                   09-JAN-2001; 2001DE-01000588
                                                                                          09-JAN-2001; 2001DE-01000588
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                                             RIBOPHARMA
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                      Limmer S,
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99.8%;
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Pred. No. 6.4e-129;
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Inhibiting expression of target genes, useful by introducing into cells two double-stranded to the target.
                                                                                               e.g.
                                                                                               for treating
that are comp
                                                                                               complementary
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Claim 13; Page 19-20; 100pp; German

The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (dsRNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAi). The method is particularly used to treat tumours or infections, especially by Plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the invention

Sequence 606 BP; 96 A; 191 C; 175 G; 144 T; 0 U; 0 Other;

Length

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Query Match
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Matches 479; Conserv
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Pred. No. 6.4e-129;
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RESULT 5
ABX09954
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5 밁 Ś 밁

ABX09954 standard; DNA; 606 ВP

АВХ09954;

23-JAN-2003 (first

Human ephrin æ DNA fragment SEQ ij 19

entry)

XXXXXXXXX Oligoribonucleotide; interferon; prion; inhibition; human; ds. oncogene; cytokine; Id; developmental;

Homo sapiens.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting expression of target genes, e.g. oncogenes, in cells, by introduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon.
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Pred. No. 6.4e-129;
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                                                                                                                                                                                                                                                          The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at complementary with that has a double-stranded structure consisting of at complementary with the target gene and has at least part of one strand stranded segment of 1-4 nt. The method provides oligoribonucleotides for but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. plasmodium or viruses/viroids, pathogenic on humans, The method provides more effective inhibition of gene expression than use increases stability and thus intracellular concentration
                                                                                                                                                                                                                              Sequence 606 BP; 96 A; 191 C; 175 G; 144 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Page 20-21; 104pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting gene expression in cells, useful for e.g. treating tumors, introducing double-stranded complementary oligoRNA having unpaired
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Pred. No. 6.4e-129;
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16-OCT-2002;
29-OCT-2002;
07-NOV-2002;
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Hafalia
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                                                                      New human receptors and membrane-associated proteins and polynucleotides for diagnosing, preventing or treating diseases associated with aberrant protein expression, e.g. cancer, atherosclerosis, AIDS, stroke or diabetes.
                                                                                                                                  WPI; 2004-316100/29.
P-PSDB; ADN02719.
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K, Gietzen K
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2002US-0417797P.
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2002US-0422375P.
2002US-0422375P.
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, Ramkumar J, Khare R,
, Swarnakar A, Lu DAM,
, KJ, Blake JJ, Ison CH;
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Tang YT, Y
Policky JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC amino acid sequences cited above; or a biologically active or immunogenic fragment of the polypeptide. The specification also discloses a naturally coccurring polynuclectide sequence that is at least 99% to at least 99% cc identical to any of the nucleotide sequences cited above; their cc complements or an RNA equivalent. The composition and methods are useful for diagnosing, preventing or treating diseases or conditions associated cwith aberrant expression of REMAP, such as cell proliferative (e.g. cancer or atherosclerosis), autoimmune/inflammatory (e.g. AIDS or cancer or atherosclerosis), addison's disease, Alzheimer's disease or stroke), developmental cor assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of REMAP. The REMAP or its fragments are call so useful in screening compounds for effectiveness as agonist or cantagonist of the polypeptides, or in altering the expression of the carget polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein interactions, drug-target interactions, and gene expression profiles. This sequence corresponds to the cDNA encoding one of the proteins of the invention.
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Matches 437
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                                      TGGCGAGGGGGGACACTCCCAGC
                                                                                 GAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCCTGGAGAGAGTGGCACATCAGGG
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  TGGCGAGGGGGGACACTCCCAGC
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98.4%;
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0; Mismatches 7;
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The invention relate protein (REMAP) and acid sequence that i

relates to novel human receptor and membrane-associated P) and the genes encoding them, a naturally-occurring amino that is at least 90% to at least 98% identical any of the

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268pp; English.

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